

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:08:53 ; Search time 19.81 Seconds
(without alignments)
236.905 Million cell updates/sec

Title: US-09-772-103-8
Perfect score: 655
Sequence: 1 MDPQVIFSLISAVILS.....CQWSSYPLTFGGTKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

all number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	68.1	129	1	P01680 mus musculus
2	444.5	67.9	108	1	KV1P_HUMAN
3	441.5	67.4	108	1	KV1V_HUMAN
4	436.5	66.6	108	1	KV1O_HUMAN
5	435.5	66.5	108	1	KV1B_HUMAN
6	434.5	66.3	108	1	KV1Y_HUMAN
7	432.5	66.0	108	1	KV1H_HUMAN
8	431	65.8	109	1	KV1T_HUMAN
9	430.5	65.7	129	1	KV1X_HUMAN
10	427.5	65.3	108	1	KV1S_HUMAN
11	427.5	65.3	129	1	KV1W_HUMAN
12	422.5	64.5	108	1	KV1F_HUMAN
13	422.5	64.5	108	1	KV1M_HUMAN
14	421.5	64.4	108	1	KV1G_HUMAN
15	421.5	64.4	108	1	KV1J_HUMAN
16	420.5	64.2	108	1	KV1A_HUMAN
17	418.5	63.9	108	1	KV1D_HUMAN
18	416	63.5	107	1	KV1L_HUMAN
19	413.5	63.1	108	1	KV1K_HUMAN
20	412.5	63.0	108	1	KV1E_HUMAN
21	412.5	63.0	108	1	KV1N_HUMAN
22	412	62.9	108	1	KV6K_MOUSE
23	409.5	62.5	108	1	KV1Q_HUMAN
24	408.5	62.4	108	1	KV1C_HUMAN
25	408.5	62.4	108	1	KV5J_MOUSE
26	408.5	62.4	117	1	KV1J_HUMAN
27	401.5	61.3	117	1	KV1I_HUMAN
28	399	60.9	107	1	KV6F_MOUSE
29	398.5	60.8	112	1	KV6I_MOUSE
30	394	60.2	107	1	KV6L_MOUSE
31	393	60.0	107	1	KV6H_MOUSE
32	393	60.0	107	1	KV6J_MOUSE
33	392	59.8	107	1	KV6J_MOUSE

34	389	59.4	133	1	KV4B_HUMAN
35	388.5	59.3	108	1	KV5K_MOUSE
36	388.5	59.3	134	1	KV4C_HUMAN
37	386.5	59.0	136	1	KV5B_MOUSE
38	385.5	58.9	108	1	KV5Q_MOUSE
39	384	58.6	129	1	KV3L_HUMAN
40	383.5	58.5	108	1	KV5L_MOUSE
41	383.5	58.5	108	1	KV5M_MOUSE
42	383.5	58.5	108	1	KV5N_MOUSE
43	383.5	58.5	149	1	KV5A_MOUSE
44	381	58.2	129	1	KV3M_HUMAN
45	379	57.9	107	1	KV6A_MOUSE

ALIGNMENTS

RESULT 1
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION S107B PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -I- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC -----
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CC -----
CC EMBL; J00577; AAA38780.1; -;
CC EMBL; V00780; CAA24157.1; -;
CC PIR; A01943; KVM57B.
CC HSP; P01679; 2FRT.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 22
CC CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
CC DOMAIN 23 45 FRAMEWORK 1.
CC DOMAIN 23 45 COMPLEMENTARITY-DETERMINING 1.
CC DOMAIN 58 57 FRAMEWORK 2.
CC DOMAIN 73 72 COMPLEMENTARITY-DETERMINING 2.
CC DOMAIN 79 79 COMPLEMENTARITY-DETERMINING 3.
CC DOMAIN 80 111 FRAMEWORK 3.
CC DOMAIN 112 118 COMPLEMENTARITY-DETERMINING 3.
CC DOMAIN 119 128 FRAMEWORK 4.
CC DISULFID 45 111 BY SIMILARITY.
CC NON_TER 129 129
CC SEQUENCE 129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;
Query Match 68.1%; Score 446; DB 1; Length 129;
Best Local Similarity 66.9%; Pred. No. 3.5e-36;

Matches 87: Conservative 21; Mismatches 18; Indels 4; Gaps 2;

1 MDFOVQIFSELLISAVILSRGDIQMTQSPSSLSASVGRVITTCSSIT--TYMSWYQ 58
 1 MDLQVQIIXELLISAVILSRGDNVITQSPAIMASLQGVKVTWCSSASSYSSYLHWYQ 60
 59 QKPKAKPLIYDTSNLASGVPRFSGSGSGTDYTLTISSLOPEDFATYYICQWSSYPLT 118
 61 QKGSAPPLIHRITSNLASGVPRFSGSGSGTYSLTISSEAEADATYYICQWSSYGP-- 118
 119 FGGTKVEIK 128
 119 FGSQTKLEIK 128

RESULT 2

ID	KVIP_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01608;			
DE	21-JUL-1986 (Rel. 01, Created)			
DE	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-I REGION ROY.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=68362076; PubMed=5595110;			
RA	Hiltschmann N.;			
RT	"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).			
RP	[2]			
RP	REVISTONS TO 39 AND 41.			
RA	Hiltschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Sugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press,			
RL	New York (1969).			
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)			
CC	MARKER.			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A01874; KLHURY.			
DR	HSP; P80362; 1WTL.			
DR	InterPro; IPR003006; Iq_MHC.			
DR	InterPro; IPR003596; Iq_v.			
DR	Pfam; PF00047; Iq; 1.			
KW	SMART; SM00406; Igv; 1.			
KW	Immunoglobulin V region; Bence-Jones protein.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DOMAIN 108 108			
FT	DISULFID 23 34			
FT	NON_TER 108			
FT	SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;			
SO				

Query Match 67.9%; Score 444.5; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 4e-36; 1; Gaps
 Matches 84; Conservative 11; Mismatches 1; Indels 1;

QY 23 DIQMTQSPSSLSASVGRVITTCSSIT-YMSWYQQKPKAPKLLIYDTSNLASGVPS 81
 DB 1 DIQMTQSPSSLSASVGRVITTCSSIT-SIFLNWYQQKPKAPKLLIYDASKLEAGVPS 60
 QY 82 RFSGSGSGTDYTLTISSLOPEDFATYYICQWSSYPLTFGGTKVEIK 128

three-dimensional structure of antibodies, in particular their combining site.";
 Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 [2]
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 MEDLINE=76039968; PubMed=1182131;
 Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
 Biochemistry 14:4943-4952(1975).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01873; KIHUE.
 DR PDB; 1REI; 17-FEB-84.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 DOMAIN 1 23
 FRAMEWORK 1.
 FT DOMAIN 24 34
 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49
 FRAMEWORK 2.
 FT DOMAIN 50 56
 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88
 FRAMEWORK 3.
 FT DOMAIN 89 97
 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107
 FRAMEWORK 4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 45 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT STRAND 108 108
 NON_TER 108
 SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 66.6%; Score 436.5; DB 1; Length 108;
 Best Local Similarity 79.2%; Pred. No. 2.3e-35;
 Matches 84; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGDRTVITCSATSS-ITVMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 DB 1 DIQMTQSPSSLSASVGDRTVITCSATSS-ITVMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 QY 82 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEI 127
 DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEI 127

RESULT 5
 KVIB_HUMAN
 ID KVIB_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION AU.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 "The structure determination of the variable portion of the Bence-Jones protein Au.";
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
 CC -!- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01862; KIHUAU.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FRAMEWORK 1.
 FT DOMAIN 24 34
 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49
 FRAMEWORK 2.
 FT DOMAIN 50 56
 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88
 FRAMEWORK 3.
 FT DOMAIN 89 97
 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 23 88
 FT NON_TER 108
 SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 66.5%; Score 435.5; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 2.9e-35;
 Matches 85; Conservative 6; Mismatches 15; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGDRTVITCSATSSIT-YMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 DB 1 DIQMTQSPSSLSASVGDRTVITCSATSSIT-YMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 QY 82 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEIK 128
 DB 61 RFGSGSGTAHFTTISLQPEDFATYYCQWSSYPLTFGGTKVEIK 107

RESULT 6
 KVIL_HUMAN
 ID KVIL_HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.,

us-09-772-103-8.rsp

Mon Jul 1 16:28:15 2002

Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 109
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 66.0%; Score 432.5; DB 1; Length 108;
 Best Local Similarity 80.4%; Pred. No. 5,7e-35;
 Matches 86; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGDRTVITCSATSI-TYMSYQKPKGKAPKLLIYDTSNLSGVPS 81
 Db 1 DIQMTQSPSSLSASVGDRTVITCSATSI-TYMSYQKPKGKAPKLLIYDTSNLSGVPS 60
 QY 82 RFGSGSGTDYTLTISSLOPEFATFYCOQWSSYPLTFGGGKVEIK 128
 Db 61 RFGSGSGTDYTLTISSLOPEFATFYCOQWSSYPLTFGGGKVEIK 107

RESULT 8
 KVIH_HUMAN STANDARD; PRT; 109 AA.

AC P01612;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION MEV.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=83081018; PubMed=6816713;
 RA Eulitz M., Linke R.P.,
 RT "Primary structure of the variable part of an amyloidogenic
 RT Bence-Jones Protein (Mev.). An unusual insertion in the third
 RT hypervariable region of a human kappa-immunoglobulin light chain."
 RT Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
 CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
 CC FOUND.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC PIR; A01879; KIHUV.
 DR HSSP; P80362; IWTLL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 98
 FT DOMAIN 99 108
 FT DISULFID 23 88
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11870 MW; B6ABF4515D55F5A0 CRC64;

Query Match 65.8%; Score 431; DB 1; Length 109;
 Best Local Similarity 78.7%; Pred. No. 8e-35;
 Matches 85; Conservative 11; Mismatches 10; Indels 2; Gaps 2;

QY 23 DIQMTQSPSSLSASVGDRTVITCSAT-SSITYMSYQKPKGKAPKLLIYDTSNLSGVPS 81

"Comparison of crystal structures of two homologous proteins:
 structural origin of altered domain interactions in immunoglobulin
 light-chain dimers."
 RL Biochemistry 33:14848-14857(1994).

RN SEQUENCE OF 1-35; PubMed=6167731;
 RX MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Wat.,"
 RL J. Mol. Biol. 147:185-193(1981).

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PDB; IWTLL; 01-NOV-94.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.

KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0AE697 CRC64;

Query Match 66.38; Score 434.5; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 3.6e-35;
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGDRTVITCSATSI-TYMSYQKPKGKAPKLLIYDTSNLSGVPS 81
 Db 1 DIQMTQSPSSLSASVGDRTVITCSATSI-TYMSYQKPKGKAPKLLIYDTSNLSGVPS 60
 QY 82 RFGSGSGTDYTLTISSLOPEFATFYCOQWSSYPLTFGGGKVEIK 128
 Db 61 RFGSGSGTDYTLTISSLOPEFATFYCOQWSSYPLTFGGGKVEIK 107

RESULT 7
 KVIH_HUMAN STANDARD; PRT; 108 AA.

AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION HAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RA "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR; A01868; KIHUV.
 DR HSSP; P80362; IWTLL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.

Db 1 DVQMTQSPSSLSASVGRVITTCRASQSSVDVLYNQKPKAPKLLIFDTSNLQSGVPS 60
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQWSSYP-LTFGGGTKVEIK 128
 Db 61 RFGSGRSGTDFTLTISLQPDFAITTCQSYTNPEVTFGGTTVDIK 108

RESULT 9
 KVIS_HUMAN
 ID KVIS_HUMAN STANDARD; PRT; 129 AA.
 AC P04432;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 MEDLINE=85014148; PubMed=6091049;
 RA Klobbeck H.G., Combriato G., Zachau H.G.;
 RT "Immunoglobulin genes of the kappa light chain type from two human
 RL lymphoid cell lines are closely related.";
 CC Nucleic Acids Res. 12:6995-7006(1984).
 CC -----
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 CC -----
 DR EMBL; X00966; CAA25478.1; ALT_TERM.
 DR PIR; A01884; KIHUHL.
 DR HSP; P80362; IWTLL.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45
 FT DOMAIN 46 56
 FT DOMAIN 57 71
 FT DOMAIN 72 78
 FT DOMAIN 79 110
 FT DOMAIN 111 119
 FT DOMAIN 120 129
 FT DISULFID 45 110
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match 65.7%; Score 430.5; DB 1; Length 129;
 Best Local Similarity 69.5%; Pred. No. 1.1e-34;
 Matches 91; Conservative 12; Mismatches 23; Indels 5; Gaps 3;
 QY 1 MDOFV--QIFSFLLISASVILSGDIQMTQSPSSLSASVGRVITTCATSSIT-YMSWY 57
 Db 1 MDMRPAQLGLLWLRLRV--RCDIQMTQSPSSLSASVGRVITTCAGHNITNLSWY 58
 QY 58 QKPGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISSLPEDFATYYCQWSSYPL 117
 Db 59 QKPGKAPKLLIYAVSNLQVGPSPRFGSGSGTAEFTLTISLQPDFAITTCQSYTNPE 118
 QY 118 TFGGGTKVEIK 128
 Db 119 TFGGGTKVDNK 129

Query Match 65.3%; Score 427.5; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 1.7e-34;
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPGKAPKLLIYDTSNLASGVPS 81
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQSSVDVLYNQKPKAPKLLIYDTSNLASGVPS 81
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQWSSYPLTFGGGTKVEIK 128
 Db 61 RFGSGSGTETLTITISLQPDFAITTCQSYTNPEVTFGGTTVDIK 107

RESULT 11
 KVIS_HUMAN
 ID KVIS_HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85014148; PubMed=6091049;
 RA Klobbeck H.G., Combriato G., Zachau H.G.;

RESULT 10
 KVIS_HUMAN
 ID KVIS_HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WES.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 RL Wes).";
 CC Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01877; KIHUWS.
 DR HSP; P80362; IWTLL.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 23 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 98
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 1.7e-34;
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPGKAPKLLIYDTSNLASGVPS 81
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQSSVDVLYNQKPKAPKLLIYDTSNLASGVPS 81
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQWSSYPLTFGGGTKVEIK 128
 Db 61 RFGSGSGTETLTITISLQPDFAITTCQSYTNPEVTFGGTTVDIK 107

RESULT 11
 KVIS_HUMAN
 ID KVIS_HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85014148; PubMed=6091049;
 RA Klobbeck H.G., Combriato G., Zachau H.G.;

Query Match 65.3%; Score 427.5; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 1.7e-34;
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPGKAPKLLIYDTSNLASGVPS 81
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQSSVDVLYNQKPKAPKLLIYDTSNLASGVPS 81
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQWSSYPLTFGGGTKVEIK 128
 Db 61 RFGSGSGTETLTITISLQPDFAITTCQSYTNPEVTFGGTTVDIK 107

us-09-772-103-8.rsp

Mon Jul 1 16:28:15 2002

Gall W.E., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";

Biochemistry 9:3188-3196(1970).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

CC PIR; A01866; KIHOU.

DR HSP; P01607; IREI.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region.

KW DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 88

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 9CD294F2F4D88823 CRC64;

Query Match 64.5%; Score 422.5; DB 1; Length 108;

Best Local Similarity 76.6%; Pred. No. 5.2e-34;

Matches 82; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCSTSI-TYMSWYQKPKAPKLLIYDTSNLASGVPS 81

Db 1 DIQMTQSPSSLSASVGRVITTCSTSI-TYMSWYQKPKAPKLLIYDTSNLASGVPS 81

QY 82 RFGSGSGDYLTLTSSLPQDFATYVCOQWSSYPLTFGGTKVEIK 128

Db 61 RFGSGSGDYLTLTSSLPQDFATYVCOQWSSYPLTFGGTKVEIK 107

RESULT 13

KVIM_HUMAN STANDARD; PRT; 108 AA.

AC P01605; 1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION LAY.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE.

RP MEDLINE=7038198; PubMed=824717;

RX Capra J.D., Kiappner D.G.;

RA "Complete amino acid sequence of the variable domains of two human

RT IGM anti-gamma globulins (Lay/Pom) with shared idiotype

RT Specificities.";

RL Scand. J. Immunol. 5:677-684(1976).

CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS

CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,

CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.

CC PIR; A01871; KIHULX.

DR HSP; P01607; IREI.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region.

KW DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DISULFIDE BOND.

RP MEDLINE=71064023; PubMed=5489770;

RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino

RT acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BOND.

RP MEDLINE=71064027; PubMed=4923144;

RX

"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";

Nucleic Acids Res. 12:6995-7006(1984).

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CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch.

CC EMBL; X00965; CAA25477.1; ALT_TERM.

DR PIR; A01883; KIHUWK.

DR HSP; P01607; IREI.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region; Signal.

KW SIGNAL 22

FT CHAIN 23 129

FT DOMAIN 23 45

FT DOMAIN 46 56

FT DOMAIN 57 71

FT DOMAIN 72 78

FT DOMAIN 79 110

FT DOMAIN 111 119

FT DOMAIN 120 129

FT DISULFID 45 110

FT NON_TER 129 129

SQ SEQUENCE 129 AA; F941FA07D4AFC2F9 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 129;

Best Local Similarity 70.2%; Pred. No. 2.1e-34;

Matches 92; Conservative 13; Mismatches 21; Indels 5; Gaps 3;

QY 1 MDFOV--QIFSLTASVTLSDGIQMTQSPSSLSASVGRVITTCSTSI-TYMSWY 57

Db 1 MDMPVPAQLGLLLWLGR--ARCDIQTQSPSSLSASVGRVITTCSTSI-TYMSWY 58

QY 58 QKPKGAPKLLIYDTSNLASGVPSRSGSGDYLTLTSSLPQDFATYVCOQWSSYPL 117

Db 59 QKPKGAPKLLIYDTSNLASGVPSRSGSGDYLTLTSSLPQDFATYVCOQWSSYPL 118

QY 118 TFGGKTVEIK 128

Db 119 TFGGKTVEIK 129

RESULT 12

KVIF_HUMAN STANDARD; PRT; 108 AA.

AC P01598;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION EU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE.

RP MEDLINE=71064023; PubMed=5489770;

RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino

RT acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BOND.

RP MEDLINE=71064027; PubMed=4923144;

RX

RESULT	15
KVIR_HUMAN	
ID	KVIR_HUMAN
STANDARD;	PRT; 108 AA.
PO1610;	
AC	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
ES	IG KAPPA CHAIN V-I REGION WEA.
DE	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	[1]
IN	SEQUENCE.

CC	Anti amino acid sequence of the Fv region of a human monoclonal IgM
RT	(protein WEH) with antibody activity against 3,4-pyruvylated
RT	galactose in Klebsiella polysaccharides K80 and K33. #;
RT	Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC	-1- MISCELLANEOUS; THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC	AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC	WALLENSTROM'S MACROGLOBULINEMIA.
DR	PIR; A01876; KIHUWE.
DR	HSP; P80362; IWLTL.
DR	InterPro; IPRO03006; Ig_MHC.
DR	InterPro; IPRO03596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	Immunoglobulin V region; Monoclonal antibody.
FT	DOMAIN 1
FT	DOMAIN 23
FT	DOMAIN 24
FT	DOMAIN 34
FT	DOMAIN 35
FT	DOMAIN 49
FT	DOMAIN 50
FT	DOMAIN 56
FT	DOMAIN 57
FT	DOMAIN 88
FT	DOMAIN 97
FT	DOMAIN 98
FT	DOMAIN 89
FT	DISULFID 107
FT	NON_TER 23
FT	NON_TER 88
FT	NON_TER 108
FT	SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

	23	1	82	61
y	DIQWOTSPSLASVSGDRVTITCSATFSS-TYMSYIQQKPKAPKLLIYDTSNLASGVPS	81		
b				
	1	DIQWOTSPSLASVSGDRVTITCSAQSGIRNDLTWYQKPGTAPKRLIYGATSLQSGVPS	60	
y				
b	82	RFGSGSGDYTLITLSSLPEDFATYIYQQQSSYPLTTEGGTKVEIK	128	
	61	RFGSGSGTEFTLITNSLPEDFATYIYCLQYSSFPFEGQTKVEIK	107	

Search completed: May 7, 2002, 12:08:53
Job time: 451 sec

RESULT	15
KVIR_HUMAN	
ID	KVIR_HUMAN
STANDARD;	PRT; 108 AA.
PO1610;	
AC	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
ES	IG KAPPA CHAIN V-I REGION WEA.
SE	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	[1]
IN	SEQUENCE.

CC	Anti amino acid sequence of the Fv region of a human monoclonal IgM
RT	(protein WEH) with antibody activity against 3,4-pyruvylated
RT	galactose in Klebsiella polysaccharides K80 and K33. #;
RT	Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC	-1- MISCELLANEOUS; THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC	AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC	WALLENSTROM'S MACROGLOBULINEMIA.
DR	PIR; A01876; KIHUWE.
DR	HSP; P80362; IWLTL.
DR	InterPro; IPRO03006; Ig_MHC.
DR	InterPro; IPRO03596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	Immunoglobulin V region; Monoclonal antibody.
FT	DOMAIN 1
FT	DOMAIN 23
FT	DOMAIN 24
FT	DOMAIN 34
FT	DOMAIN 35
FT	DOMAIN 49
FT	DOMAIN 50
FT	DOMAIN 56
FT	DOMAIN 57
FT	DOMAIN 88
FT	DOMAIN 97
FT	DOMAIN 98
FT	DOMAIN 99
FT	DISULFID 107
FT	NON_TER 23
FT	NON_TER 88
FT	NON_TER 108
FT	SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

	23	1	82	61
y	DIQWOTSPSLASVSGDRVTITCSATFSS-TYMSYIQQKPKAPKLLIYDTSNLASGVPS	81		
b				
	1	DIQWOTSPSLASVSGDRVTITCSAQSGIRNDLTWYQKPGTAPKRLIYGATSLQSGVPS	60	
y				
b	82	RFGSGSGDYTLITLSSLPEDFATYIYQQQSSYPLTTEGGTKVEIK	128	
	61	RFGSGSGTEFTLITNSLPEDFATYIYCLQYSSFPFEGQTKVEIK	107	

Search completed: May 7, 2002, 12:08:53
Job time: 451 sec

